

SCORE Search Results Details for Application 10552515 and Search Result 20080624_135827_us-10-552-515-1_copy_157_933.rag.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135827_us-10-552-515-1_copy_157_933.rag.

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GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: June 24, 2008, 15:17:27 ; Search time 267 Seconds
(without alignments)
1751.538 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPFTVPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*

8: geneseqp2004a:*
 9: geneseqp2004b:*
 10: geneseqp2005:*
 11: geneseqp2006:*
 12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	4123	100.0		933	8	ADT77664	Adt77664 Splice va
2	4123	100.0		933	11	AEL84788	Ael84788 Tumor mar
3	3739	90.7		885	10	AEB13426	Aeb13426 Human pro
4	3572	86.6		843	10	AEB13424	Aeb13424 Human pro
5	3031.5	73.5		898	4	ABG15488	Abg15488 Novel hum
6	1502.5	36.4		920	6	ADB64420	Adb64420 Human pro
7	1482.5	36.0		920	6	ABP58666	Abp58666 Human dih
8	1467.5	35.6		981	8	ADK52114	Adk52114 Human ato
9	1467.5	35.6		981	12	AEN06206	Aen06206 Human eso
10	1461.5	35.4		840	11	AEG11146	Aeg11146 Human tra
11	1456.5	35.3		960	11	AEG11142	Aeg11142 Human tra
12	1452.5	35.2		1017	12	AFB77190	Afb77190 Mouse TM-
13	1437	34.9		1003	7	ADG48280	Adg48280 Human ret
14	1412.5	34.3		913	11	AEH82071	Aeh82071 Human gna
15	1378.5	33.4		1219	4	ABB62812	Abb62812 Drosophil
16	1378.5	33.4		1219	10	AFB95185	Afb95185 Fruit fly
17	1369	33.2		910	6	ADC42854	Adc42854 REMAP pro
18	1369	33.2		910	11	AEL84658	Ael84658 Tumor mar
19	1367.5	33.2		712	11	AEG11145	Aeg11145 Human tra
20	1344	32.6		1075	4	ABB65993	Abb65993 Drosophil
21	1344	32.6		1075	10	AFC04729	Afc04729 Fruit fly
22	1159.5	28.1		1058	4	ABB65022	Abb65022 Drosophil
23	1159.5	28.1		1058	10	AFC01816	Afc01816 Fruit fly
24	1154	28.0		596	6	ADB64387	Adb64387 Human pro
25	1061.5	25.7		594	4	AAB92637	Aab92637 Human pro
26	1061.5	25.7		594	5	ABP43811	Abp43811 FLJ10261
27	1061.5	25.7		594	8	ADJ75429	Adj75429 Marker ge
28	1061.5	25.7		594	8	ADN04848	Adn04848 Antipsori
29	1061.5	25.7		594	11	AEG11143	Aeg11143 Human FLJ
30	1024.5	24.8		782	6	ADX42387	Adx42387 Human col
31	1024.5	24.8		782	7	ADT95905	Adt95905 Colon can
32	1024.5	24.8		782	8	ADQ96288	Adq96288 T cell ac
33	1024.5	24.8		782	8	ADQ96104	Adq96104 T cell ac
34	912.5	22.1		475	6	ADB64962	Adb64962 Human pro

35	873.5	21.2	642	7	ADM05798	Adm05798 Human pro
36	873.5	21.2	642	10	AEC88728	Aec88728 Human cDN
37	873.5	21.2	642	11	AEG11144	Aeg11144 Human FLJ
38	819.5	19.9	443	5	ABP41785	Abp41785 Human ova
39	784.5	19.0	390	5	ABB90382	Abb90382 Human pol
40	735	17.8	139	5	AAE24066	Aae24066 Human pro
41	722.5	17.5	360	4	AAM40391	Aam40391 Human pol
42	711.5	17.3	346	8	ADP29628	Adp29628 Human sec
43	695.5	16.9	608	8	ADQ96298	Adq96298 T cell ac
44	695.5	16.9	608	8	ADQ96286	Adq96286 T cell ac
45	684.5	16.6	483	7	ADM05305	Adm05305 Human pro

ALIGNMENTS

RESULT 1

ADT77664

ID ADT77664 standard; protein; 933 AA.

XX

AC ADT77664;

XX

DT 15-JUN-2007 (revised)

DT 13-JAN-2005 (first entry)

XX

DE Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.

XX

KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;
 KW prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;
 KW NGEP long variant; NGEP long variant [Homo sapiens]; G05886.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .345

FT /label= Cytoplasmic

FT Region 157. .933

FT /note= "An immunogenic fragment comprising 8 consecutive
 FT amino acids that specifically binds to an antibody that
 FT specifixally binds to a polypeptide comprising amino
 FT acids 157-933 is referred to in Claim 1"

FT Region 170. .178

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 215. .223

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 258. .266

FT /note= "Epitope, predicted to bind HLA2-01"

FT Domain 346. .368

FT /label= Transmembrane

FT	Domain	369. .421
FT		/label= External
FT		/note= "Cell surface"
FT	Region	403. .411
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	422. .441
FT		/label= Transmembrane
FT	Region	427. .435
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	442. .501
FT		/label= Cytoplasmic
FT	Domain	502. .524
FT		/label= Transmembrane
FT	Domain	525. .543
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	544. .566
FT		/label= Transmembrane
FT	Region	557. .565
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Region	562. .570
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	567. .586
FT		/label= Cytoplasmic
FT	Domain	587. .609
FT		/label= Transmembrane
FT	Domain	610. .714
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	715. .737
FT		/label= Transmembrane
FT	Domain	738. .761
FT		/label= Cytoplasmic
FT	Domain	762. .784
FT		/label= Transmembrane
FT	Domain	785. .933
FT		/label= External
FT		/note= "Cell surface"
FT	Region	846. .854
FT		/note= "Epitope, predicted to bind HLA2-01"
XX		
PN	WO2004092213-A1.	
XX		
PD	28-OCT-2004.	
XX		
PF	05-APR-2004; 2004WO-US010588.	
XX		
PR	08-APR-2003; 2003US-0461399P.	
XX		

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Pastan I, Bera TK, Lee B;

XX

DR WPI; 2004-758338/74.

DR N-PSDB; ADT77665.

DR PC:NCBI; gi48093524.

XX

PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.

XX

PS Claim 1; SEQ ID NO 1; 88pp; English.

XX

CC The present sequence is the protein sequence of splice variant-novel gene
CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
CC a prostate sample. Claimed methods for detecting prostate cancer in a
CC subject comprise: contacting the sample with an antibody that
CC specifically binds a SV-NGEP polypeptide and detecting the formation of
CC an immune complex; or detecting an increase in expression of SV-NGEP
CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
CC detect metastatic prostate cancer cells at locations other than the
CC prostate. A claimed method for producing an immune response against a
CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
CC comprises administering the polypeptide, or a polynucleotide encoding it,
CC to produce an immune response that decreases growth of the prostate
CC cancer. A claimed method for inhibiting the growth of a malignant cell
CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
CC cell, and contacting the malignant cell with the activated CTLs.
CC Alternatively, growth of a malignant cell is inhibited by contact with an
CC antibody that specifically binds an SV-NGEP polypeptide, where the
CC antibody is linked to an effector molecule (chemotherapeutic agent or
CC toxin) that inhibits growth of the malignant cell. This may be performed
CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
CC sample are also claimed.

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 933 AA;

Query Match 100.0%; Score 4123; DB 8; Length 933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60

Db	157	 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	216
Qy	61	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFFTSTKRHQILFEILAKTPYGHEKKNLL	120
Db	217	 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFFTSTKRHQILFEILAKTPYGHEKKNLL	276
Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	180
Db	277	 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	336
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	337	 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	396
Qy	241	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	300
Db	397	 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	456
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
Db	457	 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	516
Qy	361	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM	420
Db	517	 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM	576
Qy	421	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	480
Db	577	 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	636
Qy	481	LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY	540
Db	637	 LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY	696
Qy	541	ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	600
Db	697	 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	756
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	660
Db	757	 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	816
Qy	661	SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIP	720
Db	817	 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIP	876
Qy	721	ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	777

Db 877 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPTFTVPKASQLQQ 933

RESULT 2

AEL84788

ID AEL84788 standard; protein; 933 AA.

XX

AC AEL84788;

XX

DT 18-OCT-2007 (revised)

DT 15-JUN-2007 (revised)

DT 28-DEC-2006 (first entry)

XX

DE Tumor marker gene NGEP SEQ ID NO 155.

XX

KW cytostatic; diagnosis; prognosis; tumor marker; gene expression;

KW drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;

KW GO5886.

XX

OS Homo sapiens.

XX

PN WO2006110593-A2.

XX

PD 19-OCT-2006.

XX

PF 07-APR-2006; 2006WO-US013172.

XX

PR 07-APR-2005; 2005US-0669342P.

PR 11-OCT-2005; 2005US-0725982P.

XX

PA (MACR-) MACROGENICS INC.

XX

PI Von Haller PD, Schummer M, Meyer DW, Schubert LA, Tjoelker LW;

XX

DR WPI; 2006-814687/82.

DR N-PSDB; AEL84787.

DR REFSEQ; NP_001001891.

DR PC:NCBI; gi48093524.

XX

PT Detecting or diagnosing cancer in a subject comprises determining
PT expression of at least one gene, and comparing level of expression to a
PT control sample from a normal subject, where increased expression level
PT indicates cancer.

XX

PS Claim 8; SEQ ID NO 155; 583pp; English.

XX

CC The invention describes a method of detecting or diagnosing cancer in a
CC subject comprising determining the expression level of at least one gene,
CC and comparing the level of expression to a corresponding control sample

from a normal subject, where cancer is detected or diagnosed if there is an increase in the expression level of the gene relative to the expression in the control sample. Also described are: identifying a compound to be tested for its ability to prevent, treat, manage, or ameliorate cancer or its symptom; a compound identified by the method; treating cancer in a patient; treating a cancer in a subject that is fully or partially refractory to a first treatment in a patient; and a pharmaceutical composition comprising an amount of an antibody selected from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2, anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT, anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB, anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti-FLJ11848, anti-ENTPD2, anti-PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26, anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2, anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b antibody, and a pharmaceutical carrier. The methods are useful for detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary, prostate, pancreas, or bladder cancer. This is the amino acid sequence of NGEP, altered levels of expression are useful in the diagnosis or prognosis of cancer.

Revised record issued on 18-OCT-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 933 AA;

Query Match 100.0%; Score 4123; DB 11; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	60
Db	157	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	216
Qy	61	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	120
Db	217	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	276

Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	180
Db	277	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	336
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	337	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	396
Qy	241	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	300
Db	397	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	456
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
Db	457	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	516
Qy	361	SIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNLVFIILISKIYVSLAHVLTRWEM	420
Db	517	SIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNLVFIILISKIYVSLAHVLTRWEM	576
Qy	421	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	480
Db	577	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	636
Qy	481	LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSKKRKAGASAGASQGPWEDDY	540
Db	637	LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSKKRKAGASAGASQGPWEDDY	696
Qy	541	ELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	600
Db	697	ELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	756
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	660
Db	757	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	816
Qy	661	SSF AAAHNRTC RYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVS VGRLLDLLVPDIP	720
Db	817	SSF AAAHNRTC RYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVS VGRLLDLLVPDIP	876
Qy	721	ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	777
Db	877	ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	933

RESULT 3
AEB13426
ID AEB13426 standard; protein; 885 AA.

XX
AC AEB13426;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human prostate specific polypeptide #2.
XX
KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW cancer; prostate tumor; cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005062788-A2.
XX
PD 14-JUL-2005.
XX
PF 16-DEC-2004; 2004WO-US042406.
XX
PR 22-DEC-2003; 2003US-0531809P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Weigle B, Ebner R;
XX
DR WPI; 2005-497793/50.
DR N-PSDB; AEB13425.
XX
PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.
XX
PS Claim 12; SEQ ID NO 5; 59pp; English.
XX
CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous

state or potentially cancerous state, an antibody that reacts with a prostate specific polypeptide, an immunoconjugate comprising the antibody and a cytotoxic agent, a method of treating cancer involving contacting a cancerous cell in vivo with an agent having activity against a prostate specific polypeptide and an immunogenic composition the prostate specific polypeptide. The prostate specific polypeptide is useful for identifying an agent that modulates the activity of a cancer related gene. The immunogenic composition is useful for treating cancer, preferably prostate cancer in an animal, e.g. human, which involves administering the immunogenic composition that is sufficient to elicit the production of cytotoxic T lymphocytes specific for the prostate specific polypeptide. The invention is useful for identifying anti-neoplastic agents. This sequence represents a human prostate specific polypeptide of the invention.

XX

SQ Sequence 885 AA;

Query Match 90.7%; Score 3739; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	60
Db	158	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	217
Qy	61	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	120
Db	218	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	277
Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPAAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	180
Db	278	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPAAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	337
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	338	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	397
Qy	241	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	300
Db	398	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	457
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
Db	458	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	517
Qy	361	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM	420
Db	518	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM	577

Qy	421	HRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	480
Db	578	HRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	637
Qy	481	LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY	540
Db	638	LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY	697
Qy	541	ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	600
Db	698	ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	757
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	660
Db	758	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	817
Qy	661	SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFE	702
Db	818	SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFE	859

RESULT 4

AEB13424

ID	AEB13424 standard; protein; 843 AA.
XX	
AC	AEB13424;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	Human prostate specific polypeptide #1.
XX	
KW	Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW	cancer; prostate tumor; cytostatic; neoplasm.
XX	
OS	Homo sapiens.
XX	
PN	WO2005062788-A2.
XX	
PD	14-JUL-2005.
XX	
PF	16-DEC-2004; 2004WO-US042406.
XX	
PR	22-DEC-2003; 2003US-0531809P.
XX	
PA	(AVAL-) AVALON PHARM INC.
XX	
PI	Weigle B, Ebner R;
XX	
DR	WPI; 2005-497793/50.

Qy	61	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	120
Db	218	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	277
Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQSQVLFQHWARWGKWNKYQPLDHVR	180
Db	278	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQSQVLFQHWARWGKWNKYQPLDHVR	337
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	338	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	397
Qy	241	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	300
Db	398	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	457
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
Db	458	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	517
Qy	361	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNLVFIILILSKIYVSLAHVLTRWEM	420
Db	518	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNLVFIILILSKIYVSLAHVLTRWEM	577
Qy	421	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	480
Db	578	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	637
Qy	481	LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSKKRKAGASAGASQGPWEDDY	540
Db	638	LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSKKRKAGASAGASQGPWEDDY	697
Qy	541	ELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	600
Db	698	ELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA	757
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	660
Db	758	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	817
Qy	661	SSFAAAHNRTC	671
Db	818	SSFAAAHNRTC	828

RESULT 5
ABG15488
ID ABG15488 standard; protein; 898 AA.
XX

AC ABG15488;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #15479.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS79675.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 45847; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 898 AA;

Query Match 73.5%; Score 3031.5; DB 4; Length 898;
Best Local Similarity 91.2%; Pred. No. 6.3e-316;
Matches 578; Conservative 2; Mismatches 11; Indels 43; Gaps 2;

Qy	1	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL	60
		: :	
Db	250	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQDYPTRPPTGRPACCAWLGIPNVL	309
Qy	61	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	120
Db	310	LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL	369
Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVR	180
Db	370	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVR	429
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	430	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	489
Qy	241	CLDCPFWLLSSACALAQ---AGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW	296
Db	490	CLDCPFWLLSSACALAQVREEAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW	549
Qy	297	DCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVV	356
Db	550	DCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVV	609
Qy	357	MCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNLVFIILSKIYVSLAHVLT	416
Db	610	MCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNLVFIILSKIYVSLAHVLT	669
Qy	417	RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECA	476
Db	670	RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECA	729
Qy	477	AGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKRRKAGASAGASQGPW	536
Db	730	AGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKRRKAGASAGASQGPW	789

Qy	537	EDDYELVPCEGLFDEYLEM-----	VL	557
Db	790	EDDYELVPCEGLFDEYLEMGAGFCPNACPELVPELTEPEKARDQPEARSAGQDSRPEAVL		849
Qy	558	QFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKF		591
Db	850	QFGFVTIFVAAACPLAPLFALLNNWVEIRLDARKF		883

RESULT 6

ADB64420

ID	ADB64420	standard; protein; 920 AA.
XX		
AC	ADB64420;	
XX		
DT	15-JUN-2007	(revised)
DT	04-DEC-2003	(first entry)
XX		
DE	Human	protein encoded by clone FEBRA20031280.
XX		
KW	Human;	pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW	cell	regeneration; membrane protein; signal transduction-related protein;
KW	transcription-related	protein; osteoporosis; neurological disease;
KW	cancer;	tumour; BOND_PC; transmembrane protein 16D;
KW	transmembrane	protein 16D (eight membrane-spanning domains);
KW	transmembrane	protein 16D [Homo sapiens]; TMEM16D; FLJ34221; FLJ34272;
KW	FLJ35277;	MGC130026; unnamed protein product;
KW	unnamed	protein product [Homo sapiens].
XX		
OS	Homo	sapiens.
XX		
PN	EP1308459-A2.	
XX		
PD	07-MAY-2003.	
XX		
PF	28-MAR-2002;	2002EP-00007401.
XX		
PR	05-NOV-2001;	2001JP-00379298.
PR	25-JAN-2002;	2002US-0350978P.
XX		
PA	(HELI-)	HELIX RES INST.
PA	(REAS-)	RES ASSOC BIOTECHNOLOGY.
XX		
PI	Isogai T,	Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J,	Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N,	Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX		
DR	WPI;	2003-450961/43.
DR	N-PSDB;	ADB62450.

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Qy	115	EKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQAPRLNQ	RQVLFQHWARWGKWNKYQ	174
		: :: : ::	: ::	
Db	240	EGKNKIGLNRLLTNGSYEAAFPPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ		299
Qy	175	PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGT	LVFLVGCFLVFS	DIPTQELCGSKDS
		: : :	: : : :	
Db	300	PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDI		359
Qy	235	FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA		293
		: : : : : : : : :		
Db	360	I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFM	AVWATVFLEFWKRRRAVIA	418
Qy	294	YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVMV		352
		: : : : : : : : :		
Db	419	YDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSR	LIVSASGIFFMI	478
Qy	353	AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIASLTGSV	--NLVFILIL	404
		: : : : : : : : : : : : :		
Db	479	CVVIAAVFGIVIYRVVTV-----STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL		530
Qy	405	SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVN	FYSSPVYIAFFKGRFVGYPGNY	464
		: : : : : : : : : : : : : : :		
Db	531	NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVN	LSSTFYIAFFLGRFTGHPGAY	590
Qy	465	HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	LIPKLKGWWQKFRLRSKKR	523
		: : : : : : : : :		
Db	591	LRLINRWRLEECHPSGCLIDL	CMQMGIIIMVLKQTWNNFMELGYPLIQNW	WTR--RKVRQ
Qy	524	KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGF	VTIFVAACPLAPL	FALLNNW
		:		
Db	648	EHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGF	TTIFVAAFPLAPLLALLNNI	707
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR		641
		: : : : : : : :		
Db	708	IEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVIAITSDFIPRLVYA		767
Qy	642	W-----TRAHDLRGFLNFTLA-----RAPSSFAAAHNRTC	RYRAFR	677
		: : : : : : : : : : : : : :		
Db	768	YKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPE	SDGSEFSGTPLKYCRYRDYR	827
Qy	678	DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVF	SVGRLLDLLVPDIPESVEIKVKREYY	732
		: : : : : : : : : : : :		
Db	828	DPPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLISY	LIPDLPKDLRDRMRREKY	887
Qy	733	LAKQALAENEVLFGTNGTKDEQPKGSELSSHW		764
		: : : : : : : : : :		
Db	888	LIQEMMYEAELERLQKERKERKKN	GKAHHNEW	919

RESULT 7

ABP58666

ID ABP58666 standard; protein; 920 AA.

XX

AC ABP58666;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human dihydropyrimidinase related protein 1-101.20.

XX

KW Human; dihydropyrimidinase related protein 1-101.20;

KW recombinant production; gene therapy; psychosis; development disorder;

KW uracil-related metabolic disorder; thymine-related metabolic disorder;

KW pyrimidine metabolic disorder.

XX

OS Homo sapiens.

XX

PN CN1364894-A.

XX

PD 21-AUG-2002.

XX

PF 10-JAN-2001; 2001CN-00105195.

XX

PR 10-JAN-2001; 2001CN-00105195.

XX

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2003-000532/01.

DR N-PSDB; ABZ57080.

XX

PT New polypeptide-human dihydropyrimidinase relative protein 1-101, 20 and
PT polynucleotide for encoding such polypeptide.

XX

PS Claim 1; Page 28-30 (Disclosure); 36pp; Chinese.

XX

CC The invention relates to human dihydropyrimidinase related protein 1-
CC 101.20 (ABP58666) and nucleic acids encoding it (ABZ57080). The protein
CC has a molecular weight of 101.2 kD. The invention also relates to a
CC method for the recombinant production of the protein, an antagonist of
CC the protein, and the use of the protein, gene and antagonist in
CC therapeutic applications. Dihydropyrimidinase related protein 1-101.20
CC can be used in the treatment of a variety of diseases such as psychosis,
CC development disorders and uracil- and thymine-related metabolic
CC disorders. The present sequence represents human dihydropyrimidinase
CC related protein 1-101.20

XX

SQ Sequence 920 AA;

Query Match 36.0%; Score 1482.5; DB 6; Length 920;
Best Local Similarity 40.0%; Pred. No. 3.6e-149;
Matches 325; Conservative 146; Mismatches 272; Indels 69; Gaps 20;

Qy	8	NTTVHYALLSASWAVLCYYAEDLRLKLPLQE----	LPNQASNWS-----	AGLLAWLGIP	57
		: : : : : : : :			
Db	122	NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRFRRWLPKK			181
Qy	58	NVLL--EVVPDVPP-EYYSRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH			114
		: : : : : : : : : : :			
Db	182	PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA	TRSRIVHHILQRIKY-E		239
Qy	115	EKKNLLGIHQLLAEGVLSAAAFPLHDGPFKTPPEGPQAPRLNQ	RQVLFQHWARWGKWNKYQ		174
		: : : : : : : :			
Db	240	EGKNKIGLNRLLTNGSYEAAAFPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ			299
Qy	175	PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFS	DIPTQELCGSKDS		234
		: : : :			
Db	300	PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDI			359
Qy	235	FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA			293
		: : : : : :			
Db	360	I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMVAVWATVFLEFWKRRRAVIA			418
Qy	294	YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV			352
		: : : : :			
Db	419	YDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMI			478
Qy	353	AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----	SRIASLTGSVV--NLVFILIL		404
		: : : : : : : :			
Db	479	CVVIAAVFGIVIYRVVTV-----	STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL		530
Qy	405	SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNY			464
		: : : : : : :			
Db	531	NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLSSTFYIAFFLGRFTGHPGAY			590
Qy	465	HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKR			523
		: : : : : : : :			
Db	591	LRLINRWRLLEECHPSGCLIDLQMGIIMVLKQTWNNFMELGYPLIQNWTR--	RKVRQ		647
Qy	524	KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW			581
		:			
Db	648	EHGPERKISFPQWEKDYNLQPMNAYGLYDEYLEMILQFGFTTIFVAAFPLAPLLALLNNI			707
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR			641
		: : : : : : : :			
Db	708	IEIRLDAYKFVTQWRRPLASRAKDIGIGYGILEGIGILSVITNAFVIAITSDFIPRLVYA			767

Qy	642	W-----TRAHDLRGFLNFTLA-----RAPSSFAAAHNRTCryRAFR	677
	:	: :: : :	: : :
Db	768	YKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDYR	827
Qy	678	DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVFsvGRLLDLLVPDIPESVEIKVKREYY	732
		: : :: : : : : :: : : : ::	
Db	828	DPPHSLVPYGYTLQFWHVLAAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKY	887
Qy	733	LAKQALAENEVLFGTNGTKDEQPKGSELSSHW	764
	:: : : : : :		
Db	888	LIQEMMYEAELERLQKERKERKKNNGKAHHNEW	919

RESULT 8

ADK52114

ID	ADK52114 standard; protein; 981 AA.
XX	
AC	ADK52114;
XX	
DT	15-JUN-2007 (revised)
DT	20-MAY-2004 (first entry)
XX	
DE	Human atopic dermatitis/psoriasis-associated protein #29.
XX	
KW	Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
KW	antipsoriatic; rash; BOND_PC; transmembrane protein 16C;
KW	chromosome 11 open reading frame 25;
KW	transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW	transmembrane protein 16C (eight membrane-spanning domains);
KW	hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW	GO16021; GO4185; GO7001.
XX	
OS	Homo sapiens.
XX	
PN	WO2004016785-A1.
XX	
PD	26-FEB-2004.
XX	
PF	06-AUG-2003; 2003WO-JP009999.
XX	
PR	06-AUG-2002; 2002JP-00229319.
PR	14-MAY-2003; 2003JP-00136544.
XX	
PA	(GENO-) GENOX RES INC.
PA	(UYJU-) UNIV JUNTENDO.
XX	
PI	Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
PI	Mitsuishi K;

XX
DR WPI; 2004-214514/20.
DR N-PSDB; ADK52028.
DR PC:NCBI; gi13899227.
DR PC:SWISSPROT; Q9BYT9.
XX
PT Detecting atopic dermatitis or psoriasis comprises assaying levels of
PT expression of an indicator gene at a rash site and non-rash site of a
PT person with atopic dermatitis or psoriasis.
XX
PS Example 2; SEQ ID NO 147; 484pp; Japanese.
XX
CC The invention relates to detecting atopic dermatitis or psoriasis
CC comprising assaying the levels of expression of an indicator gene at a
CC rash site and non-rash site of a person with atopic dermatitis or
CC psoriasis, comparing these levels with those of a healthy person, and
CC determining that if the levels of indicators are higher or lower, then
CC this indicates the disease. Also included are a reagent for detecting
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a
CC transgenic non human vertebrate animal models for the diseases, an agent
CC for inducing the diseases in mice and a DNA chip for assaying for the
CC indicator genes. The method is used for treatment, detection and animal
CC models for research of atopic dermatitis and psoriasis. The present
CC sequence is a protein encoded by an indicator gene of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 981 AA;

Query Match 35.6%; Score 1467.5; DB 8; Length 981;
Best Local Similarity 40.9%; Pred. No. 1.6e-147;
Matches 313; Conservative 149; Mismatches 245; Indels 59; Gaps 21;

Qy 20 WAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNVLLE--VVPDV 67
| || ||| | ::| : : : : |: ::|: ||:
Db 214 WDTLCKYAERLNIRMPFRKKCYTDGRSKSMGRMQTYFRRIKDWMAQNPMVLDKSAFPDL 273

Qy 68 -PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ 124
: |: | :: |: :|:||||: : |: : : |: | | | :||:
Db 274 EESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK--VGIRK 329

Qy 125 LLAEGVLSAAFPPLHDGPFKT---PPEGPQAPRLNQVRQVLFQHWARWGKWNKYQPLDHVR 180
|: | |||| |:| ::| || | |: :|: |||| | |:|||| :|
Db 330 LINNGSYIAAFPPEHAYKSSQPIKTHGPQ---NNRHLLYERWARWGMWYKHQPLDLIR 385

Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
|||||: |||||:|:| |:|:|:| || | | : : :|:|: : : | ||||
Db 386 LYFGEKIGLYFAWLGWYTGMILPAAIVGLCVFFYGLFTMNNSQVSQEICKATEVF-MCPL 444

Qy	241	C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCS	299
		: : : : : : : : : : : :	
Db	445	CDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLEFWKRRRSILTYTWDLI	504
Qy	300	DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFFPERSRARRMLAGSVVIVVMVAVVVMC	358
		: : : : : : : :	
Db	505	EWEEEEETLRPQFEAKYKMEIVNPITGKPEPHQPSDDKVTRLVSVSGIFFMISLVITA	564
Qy	359	LVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSKIYVSLAHVLT	416
		: : : : : : : : : : : : : : :	
Db	565	VFGVVVYRLVVMEQFASFKNWFIKQYW--QFATSAAAVCINFIIIMLLNLAYEKIAYLLT	622
Qy	417	RWEMHRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC	475
		: : : : : : :	
Db	623	NLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNKLFDRWRLEEC	682
Qy	476	AAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGP	535
		: : : : : : :	
Db	683	HPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KRGIH-DASIPQ	736
Qy	536	WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFA LLNNWVEIRLDARKFVC	593
		:	
Db	737	WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVT	796
Qy	594	EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW-----T	643
		: : : : : : : : : :	
Db	797	QWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYKYGPCANHVEP	856
Qy	644	RAHDLRGFLNFTLARAP-SSFAAAHNRTCryRAFR----DDDGHYsQTYWNLLAIRLAF	697
		: : : : : :	
Db	857	SENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQYWHILAAARLAF	916
Qy	698	VIVFEHVVFsvGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV	743
		: : : : : : : : : : : :	
Db	917	IIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLvQEMMYEAEI	962

RESULT 9
AEN06206
ID AEN06206 standard; protein; 981 AA.
XX
AC AEN06206;
XX
DT 15-JUN-2007 (revised)
DT 22-FEB-2007 (first entry)
XX
DE Human esophageal cancer-associated protein SEQ ID NO 231.
XX

KW diagnostic; metastasis; esophagus tumor; gastrointestinal disease;
KW neoplasm; cytostatic; cancer; AXL; ZBTB11; TNFRSF14; NSUN5; SPEN; LTBP3;
KW SYNGR1; SLC13A1; MAP3K12; GLYAT; ZNF659; B4GALT2; POGK; AQP3; CAPG;
KW SLIT2; BOND_PC; transmembrane protein 16C;
KW chromosome 11 open reading frame 25;
KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW transmembrane protein 16C (eight membrane-spanning domains);
KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW GO16021; GO4185; GO7001.
XX
OS Homo sapiens.
XX
PN WO2006118308-A1.
XX
PD 09-NOV-2006.
XX
PF 02-MAY-2006; 2006WO-JP309177.
XX
PR 02-MAY-2005; 2005JP-00134530.
PR 13-SEP-2005; 2005JP-00265645.
PR 13-SEP-2005; 2005JP-00265678.
XX
PA (TORA) TORAY IND INC.
PA (KYOU) UNIV KYOTO.
XX
PI Akiyama H, Kozono S, Myomoto A, Nomura O, Nobumasa H, Tanaka Y;
PI Tomoda S, Shimada Y, Tsujimoto G;
XX
DR WPI; 2007-110304/11.
DR PC:NCBI; gi13899227.
DR PC:SWISSPROT; Q9BYT9.
XX
PT Composition for determining occurrence/metastasis of esophageal cancer in
PT subject, comprises an antibody binding to a polypeptide encoded by a
PT polynucleotide having a sequence of genes e.g. AXL, ZBTB11 and TNFRSF14,
PT and/or polynucleotides.
XX
PS Claim 1; SEQ ID NO 231; 142pp; Japanese.
XX
CC This invention describes a novel composition for detecting metastasis of
CC esophageal cancer in a test subject. The composition contains a probe
CC derived from polynucleotides AXL, ZBTB11, TNFRSF14, NSUN5, SPEN, LTBP3,
CC SYNGR1, SLC13A1, MAP3K12, GLYAT, ZNF659, B4GALT2, POGK, AQP3, CAPG,
CC SLIT2, their variants or fragments and an antibody. The invention also
CC claims: a) a kit for detecting, determining or presuming the occurrence
CC or metastasis of esophageal cancer in a test subject; b) a DNA chip for
CC detecting, determining or presuming the occurrence or metastasis of
CC esophageal cancer and c) a method to detect, determine or presume the
CC occurrence or metastasis of esophageal cancer in a test subject by

CC detecting the presence of or amount or expression level of one or more
CC esophagus-cancer related target nucleic acid in a biological sample. The
CC method enables the rapid and convenient detection of occurrence or
CC metastasis of esophageal cancer in test subject with high sensitivity.
CC This sequence represents a protein used in the method of the invention
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 981 AA;

Query Match 35.6%; Score 1467.5; DB 12; Length 981;
Best Local Similarity 40.9%; Pred. No. 1.6e-147;
Matches 313; Conservative 149; Mismatches 245; Indels 59; Gaps 21;

Qy 20 WAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNVLLE--VVPDV 67
| || ||| |::| : : : : |: ::|: ||:
Db 214 WDTLCKYAERLNIRMPFRKKCYITDGRSKSMGRMQTYFRRIKDWMAQNPMVLDKSAFPDL 273

Qy 68 -PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ 124
: |: | :: |: :|:||||: : |:|: :| :| | | :|| :
Db 274 EESDCYTGPFSRARIHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK--VGIRK 329

Qy 125 LLAEGVLSAAFPLHDGPFKT---PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
|: | |||| |:| ::| || | | :|:| |||| | |:| ||| :|
Db 330 LINNGSYIAAFPPHEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMWYKHQPLDLIR 385

Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
||||: ||||| |:| |:|:| | | | : : :|:| : : | ||||
Db 386 LYFGEKIGLYFAWLGWYTGM LIPAAIVGLCVFFYGLFTMNSQVSQEICKATEVF-MCPL 444

Qy 241 C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCS 299
| :| |: :| |: |||:|||||:|:|:| : |:|:|: : | | ||
Db 445 CDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLEFWKRRRSILTYTWDLI 504

Qy 300 DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMC 358
::|: || |||| | | ||||: |:| : |:| | |::|:
Db 505 EWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGIFFMISLVITA 564

Qy 359 LVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSKIYVSLAHVLT 416
: ::|| :| | | : | :| :| :|:| :| :|:|
Db 565 VFGVVYRLVMEQFASFKNFIKQYW--QFATSAAVCINFIIIMLLNLAYEKIAYLLT 622

Qy 417 RWEMHRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC 475
| ||:::|:| ||:|:|||| || ||||| ||||:| |: || | |||
Db 623 NLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNKLFDRWRLEEC 682

Qy 476 AAGGCLIELAQELLVIMVGKQVINNMQEV LIPKLGWWQKFRLRSKKRKAGASAGASQGP 535
||||:| :: ||| ||: || |: | :: || : :: | | ||

Db	683	HPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KRGIH-DASIPQ	736
Qy	536	WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVC	593
		: : :	
Db	737	WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVT	796
Qy	594	EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW-----T	643
		: : : : : : : :	
Db	797	QWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYKYGPCANHVEP	856
Qy	644	RAHDLRGFLNFTLARAP-SSFAAAHNRTCryRAFR----DDGDHYSQTYWNLLAIRLAF	697
		: : : : : : : : : :	
Db	857	SENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQYWHILAAARLAF	916
Qy	698	VIVFEHVVFVSGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV	743
		: : : : : : : : :: : : :	
Db	917	IIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEAE	962

RESULT 10

AEG11146

ID	AEG11146 standard; protein; 840 AA.
XX	
AC	AEG11146;
XX	
DT	15-JUN-2007 (revised)
DT	20-APR-2006 (first entry)
XX	
DE	Human transmembrane protein 16A, SEQ ID NO: 11.
XX	
KW	Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW	cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW	TMEM16A protein; TMEM16A protein [Homo sapiens].
XX	
OS	Homo sapiens.
XX	
PN	US2006040292-A1.
XX	
PD	23-FEB-2006.
XX	
PF	08-JUL-2005; 2005US-00177894.
XX	
PR	08-JUL-2004; 2004US-0586676P.
XX	
PA	(WEST/) WEST R B.
PA	(VRIJ/) VAN DE RIJN M.
XX	
PI	West RB, Van De Rijn M;
XX	

```
XX
PT   Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT   positive subclass, involves detecting expression or activity of gene
PT   encoding DOG1 polypeptide in sample.
```

XX
PS Disclosure; SEQ ID NO 11; 177pp; English.

XX The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX
SQ Sequence 840 AA;

Query Match 35.4%; Score 1461.5; DB 11; Length 840;
Best Local Similarity 40.1%; Pred. No. 5.6e-147;
Matches 331; Conservative 149; Mismatches 260; Indels 85; Gaps 21;

Qy	5	QDGNTTVH---YALLSASWAVLCYYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLL	61
		: : : : : : : :: : : :	
Db	28	RDEDTKIHGVGFVKIHAPWNVLCREAEFLKCLKMPTKKMYH--INETRGLLK--KINSVLQ	83
Qy	62	EVVPDVPPEYYSCR-----FRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	111
		:: : : : : : :	
Db	84	KITDPIQPKVAEHRPQTMKRLSYPFSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT	142
Qy	112	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQQRQVLFQHWARWGKWN	171
		: : : : : : :: : : :	
Db	143	CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY	196
Qy	172	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	231
		: : : : :: : : : : :	
Db	197	KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ	256

Qy	232	KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA	290
Db	257	RHNITMCPLCDKTC SYWKMS SACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM	316
Qy	291	TLAYRWDCSDYEDTEERPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGS	345
Db	317	RLNYRWDLTGFEEDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNL	374
Qy	346	VVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAWASRIASLTGSVNVNLVFILILS	405
Db	375	VSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLD	434
Qy	406	KIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYH	465
Db	435	EVYGCJARWLTKIEVPKTEKSFEERLIFKAFLKLVNSYTPIFYVAFFKGRFVGRPGDYV	494
Qy	466	TLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQEVLIPKLKGWWQKFRRLRSKKR	523
Db	495	YIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLKQQSP	554
Qy	524	KAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVE	583
Db	555	PDHEECVKKRQRYEVDYNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLNNIIE	614
Qy	584	IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRA--YYR	641
Db	615	IRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIGKLAVIIDAFVISFTSDFIPRLVYLYM	674
Qy	642	WTRAHDLRGFLNFTLARAPSSF-----AAAHN-----RTCryRAFRD---DDGH	682
Db	675	YSKNGTMHGfVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSENK	730
Qy	683	Y--SQTYWNLLAIRLAFVIVFEHVVFsvGRLLDLLVPDIPESVEIKVKREYYLA-----	734
Db	731	YDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQqIHKEKVLmVELFMR	790
Qy	735	----KQALAENEVLFGTNGTKDEQP-----KGSELSSH	763
Db	791	EEQDKQQLL--ETCMEKERQKDEPPCNHHNTKACPDSLGSPPASH	833

RESULT 11
AEG11142
ID AEG11142 standard; protein; 960 AA.
XX
AC AEG11142;
XX
DT 15-JUN-2007 (revised)
DT 20-APR-2006 (first entry)

XX
DE Human transmembrane protein 16A, SEQ ID NO: 7.
XX
KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW transmembrane protein 16A;
KW transmembrane protein 16A (eight membrane-spanning domains);
KW oral cancer overexpressed 2; membrane protein;
KW tumor amplified and overexpressed sequence 2;
KW transmembrane protein 16A [Homo sapiens]; TMEM16A; TAOS2; ORAOV2;
KW FLJ10261.
XX
OS Homo sapiens.
XX
PN US2006040292-A1.
XX
PD 23-FEB-2006.
XX
PF 08-JUL-2005; 2005US-00177894.
XX
PR 08-JUL-2004; 2004US-0586676P.
XX
PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX
DR WPI; 2006-182760/19.
DR N-PSDB; AEG11136.
DR REFSEQ; NP_060513.
DR PC:NCBI; gi40354210.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 7; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by

CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 960 AA;

Query Match 35.3%; Score 1456.5; DB 11; Length 960;
Best Local Similarity 40.2%; Pred. No. 2.4e-146;
Matches 333; Conservative 147; Mismatches 260; Indels 89; Gaps 22;

Qy	5	QDGNTTVH---YALLSASWAVLCYYAEDLRCLKPLQELPNQASNWSAGLLAWLGIPNVLL	61
		: : : : : : : : : : : :	
Db	144	RDEDTKIHGVGFVKIHAPWNVLCREAEFLKCLKMPTKKMYH--INETRGLLK--KINSVLQ	199
Qy	62	EVVPDVPPEYYSCR-----FRVKNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	111
		:: : : : : : : :	
Db	200	KITDPIQPKVAEHRPQTMKRLSYPFSSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT	258
Qy	112	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWN	171
		: : : : : : : : : : :	
Db	259	CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY	312
Qy	172	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	231
		: : : : : : : : : : :	
Db	313	KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ	372
Qy	232	KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA	290
		: : : : : :	
Db	373	RHNITMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM	432
Qy	291	TLAYRWDCSDYEDTEE---RPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRM	341
		: : : : : :	
Db	433	RLNYRWDLTGFEETEEAVKDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAY	490
Qy	342	LAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVVNLVFI	401
		: : : : : : : : : : : : : :	
Db	491	LTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVI	550
Qy	402	LILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYP	461
		:: :: : : : : : : : : : :	
Db	551	ILLDEVYGCARWLTKIEVPKTEKSFEERLIFKAFLKLVNSYTPIFYVAFFKGRFVGRP	610
Qy	462	GNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLR	519
		: : : : : : : : : :	
Db	611	GDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLK	670
Qy	520	SKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLN	579
		: : : : : : : :	

Db	671	QQSPPDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLN	730
Qy	580	NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRA-	638
		: : : : :	
Db	731	NIIEIRLDAKKFVTELRPVAVRAKDIGIWYNILRGIGKLAVIINAFVISFTSDFIPRLV	790
Qy	639	-YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN-----RTCRYRAFRD---	678
		: : : : : : : : :	
Db	791	YLYMYSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPW	846
Qy	679	DDGHY--SQTYWNLLAIRLAFVIVFEHVVF'SVGRLLDLLVPDIPESVEIKVKREYYLA--	734
		: : : : : : : : : : : : : :	
Db	847	SENKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHKEKVLME	906
Qy	735	-----KQALAENEVLFGTNGTKDEQP-----KGSELSSH	763
Db	907	LFMREEQDKQQLL--ETWMEKERQKDEPPCNHHNTKACPDSLGSPAPSH	953

RESULT 12

AFB77190

ID	AFB77190 standard; protein; 1017 AA.
XX	
AC	AFB77190;
XX	
DT	28-JUN-2007 (first entry)
XX	
DE	Mouse TM-1 (Tmem16a) protein.
XX	
KW	Cell isolation; stem cell; therapeutic; transgenic animal; screening;
KW	tissue regeneration; genitourinary disease; uropathic;
KW	intervertebral disk displacement; degeneration; injury; vulnerary;
KW	back pain; transmembrane factor-1; Tmem16a.
XX	
OS	Mus musculus.
XX	
PN	WO2007027583-A2.
XX	
PD	08-MAR-2007.
XX	
PF	28-AUG-2006; 2006WO-US033491.
XX	
PR	31-AUG-2005; 2005US-0713400P.
XX	
PA	(UYFL) UNIV FLORIDA RES FOUND INC.
XX	
PI	Harfe BD, Cohn MJ;
XX	
DR	WPI; 2007-412931/39.

DR N-PSDB; AFB77189.
XX
PT Isolating sonic hedgehog expressing-cells comprises obtaining a non-human
PT transgenic subject in which a marker gene has been inserted into the
PT subject's genome.
XX
PS Disclosure; SEQ ID NO 2; 96pp; English.
XX
CC The present invention relates to a method of isolating cells in selected
CC tissues co-expressing the sonic hedgehog (Shh) gene and a marker gene.
CC The method involves obtaining a non-human transgenic subject in which a
CC marker gene has been inserted into the subject's genome and isolating
CC Shh/marker gene expressing cells and Shh/marker gene non-expressing cells
CC from the selected tissue. The invention further provides a method of
CC identifying differentially expressed genes (e.g. transmembrane factors TM
CC -1 and TM-2, EST 1437418, Mmu-miR-135a-2 and AP-2 beta) in selected
CC tissues co-expressing the sonic hedgehog gene and a marker gene. The
CC invention is useful in tissue engineering, regeneration, reconstruction
CC and/or repair of tissues and genitourinary system and also in treating
CC intervertebral disk rupture, degeneration, disease or injury and back
CC pain. The invention is further useful for generating transgenic animal.
CC The present sequence is the mouse TM-1 (Tmem16a) protein.
XX
SQ Sequence 1017 AA;

Query Match 35.2%; Score 1452.5; DB 12; Length 1017;
Best Local Similarity 40.0%; Pred. No. 7e-146;
Matches 330; Conservative 156; Mismatches 257; Indels 81; Gaps 22;

Qy 6 DGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLL 62
| :| :| : : | | || | | :||:| : :: : : : : ||| | :|| :
Db 202 DEDTKIHGVGFVKIHAPWHVLCREAEFLKLKMPTKKVYHISE--TRGLLK--TINSVLQK 257

Qy 63 VVPDVPPEYYSCRFRVNKLPRFLGS-----DNQDTFFTSTKRHQILFEILAKTPYG 113
: : | : | : | : :||| | | | :||| :|
Db 258 ITDPIQPKVAEHRPQTTKRLSYFSSREKQHLFDLTDRDSFFDSKTRSTIVYEILKRTTCT 317

Qy 114 HEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWNKY 173
| : :|| ||| || |||:|||| : || | | :||:| || :| : ||
Db 318 KAKYS-MGITSLLANGVYSAAYPLHDGDY----EGDNV-EFNDRKLLYEAWASYGVFYKY 371

Qy 174 QPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKD 233
||:| ||:||||| ||||| || | :||:| || :|| | | :||:| :| :
Db 372 QPIDLVRKYFGEKVGLYFAWLGAYTQMLIPASIVGVIVFLYGCATVDENIPSMEMCDQRY 431

Qy 234 SFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATL 292
: ||||| | :| :||||| :| |||: |||||:||||| :||| | |
Db 432 NITMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQMRL 491

Qy	293	AYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLA	343
		: : : : : : :	
Db	492	NYRWDLTGFEEDDAAVKDHPRAEYEARVLEKSLRKESRNKET--DKVKLTWRDRFPAYFT	549
Qy	344	GSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVVNLVFILI	403
		: : : : : : : : : : : : : : :	
Db	550	NLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNIRVTVTATAVIINLVVIIL	609
Qy	404	LSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGN	463
		: : : : : : : : : : : : : : :	
Db	610	LDEVYGCIARWLTKIEVPKTEKSFEERLTFKAFLKLVNSYTPIFYVAFFKGRFVGRPGD	669
Qy	464	YHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLPKLGKWWQKFRRLRSK	521
		: : : : : : : : : : : : :	
Db	670	YVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKFIRYLKLRRQ	729
Qy	522	KRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW	581
		: : : : : : : : : : : :	
Db	730	SPSDREEYVVRKQRYEVDNFLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLNNI	789
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR	641
		: : : : : : : : : : :	
Db	790	IEIRLDAKKFVTELRRPVAIRAKDIGIWYNILRGVGKLAVIINAFVISFTSDFIPRLVYL	849
Qy	642	WTRAHD--LRGFLNFTLARAPSSF-----AAAHN-----RTCRYRAFRD---DD	680
		: : : : : : : : : : : :	
Db	850	YMYSQNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSE	905
Qy	681	GHY--SQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIPESVEIKVKREYYL-----	733
		: : : : : : : : : : : : :	
Db	906	HKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQIQHKEKVLMLVELF	965
Qy	734	-----AKQALAENEVLFGTNGTKDEQPKGSELSSHWTPTVTPKA	772
		: : : : : : : :	
Db	966	MREEQGKQQLLDTWM-----EKEKPRDVPCNNH-SPTTHPEA	1001

RESULT 13

ADG48280

ID ADG48280 standard; protein; 1003 AA.

XX

AC ADG48280;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human retina-specific protein - C12orf3variants.

XX

KW human; retina-specific protein; NETO1; retinal disease;

KW age related macular degeneration; night blindness; C12orf3variants.

XX
OS Homo sapiens.
XX
PN WO2003068967-A2.
XX
PD 21-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001625.
XX
PR 18-FEB-2002; 2002EP-00003675.
PR 21-FEB-2002; 2002US-0357857P.
XX
PA (LYNK-) LYNKEUS BIO TECH GMBH.
XX
PI Stoehr BH, Weber FHB, Goehring F;
XX
DR WPI; 2003-767334/72.
DR N-PSDB; ADG48279.
XX
PT New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.
XX
PS Claim 18; Fig 14; 199pp; English.
XX
CC The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NET01. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents the human retina-specific protein
CC C12orf3variants.
XX
SQ Sequence 1003 AA;

Query Match 34.9%; Score 1437; DB 7; Length 1003;
Best Local Similarity 38.7%; Pred. No. 3.2e-144;
Matches 326; Conservative 161; Mismatches 263; Indels 92; Gaps 23;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQ-----ASNWSAGLLAW 53
:|::: : : | | | | | :|:|:| : : : | :|| |
Db 174 EKDLNKSQGSIFVRIHAPWQVLAREAEFLKIKVPTKKEMYEIKAGGSIAKKFSAAAL--- 230

Qy 54 LGIPNVLLEVPDPPEYYSCRFRVNKLP-----RFLGSDNQDTFFTSTKRHQILFEIL 107
: : | | | : : : : | :||| : | :|: |||
Db 231 ---QKLSSHLQPRV-PEHSNNKMKNLSYPFSREKMYLYNIQEKDTFFDNATRSRIVHEIL 286

Qy 108 AKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARW 167
:| :|:|: |:| : ||:|||| : :| : :| |:|:| |||:
Db 287 KRTACS-RANNTMGINSLIANNIYEAAYPLHDGEYDSPEDD-----MNDRKLLYQEWARY 340

Qy	168	GKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQE	227
		: : : : : : : : : : : : : : :	
Db	341	GVFYKFQPIDLIRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVIVFLYGCATIEEDIPSRE	400
Qy	228	LCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWK	286
		: ::: : : : : : : : :	
Db	401	MCDQQNAFTMCPLCDKSCDYWNLSSACGTAQASHLFDNPATVFFSIFMALWATMFLENWK	460
Qy	287	RKSATLAYRWDCSDYEDTEER----PRPQFAA-----SAPMTAPNPIT----G	326
		: : : :	
Db	461	RLQMRLGYFWDLTGIEEEEEERAQEHRSPEYETKVREKMLKESNQSAVQKLETNTTECGDE	520
Qy	327	EDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWAS	386
		: : : : : : : : : : : : : : :	
Db	521	DDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITTAAALS-----LNKATRS	575
Qy	387	RI---ASLTGSVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNF	443
		: : ::: : : : : : : : : : : : :	
Db	576	NVRVTVTATAVIINLVVILILDEIYGAVAKWLTKIEVPKTEQTFEERLILKAFLKLVNA	635
Qy	444	YSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNM	501
		: : : : : : : : : : : : :	
Db	636	YSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELCIQLSIIMLGKQLIQNNI	695
Qy	502	QEVLPKPKLKGWWQKFRLRSKKRKAGASAGA-SQGP--WEDDYELVPCEGLFDEYLEMVLQ	558
		: : : : : : : : : : : : : : :	
Db	696	FEIGVPKLK---KLFRKLKDETEAGETDSAHSKHPEQWDLTDYSLEPYTGLTPEYMEMIIQ	752
Qy	559	FGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH	618
		: : : : : : : : : : : : : :	
Db	753	FGFVTLFVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPDVRTKDIGIWFIDILSGIGK	812
Qy	619	LAVISNAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLA-----RAPSSFAA	665
		: : : : : : : : : : : : : : :	
Db	813	FSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFEVNHTLSFFNVSQLKEGTQPEN SQFD	872
Qy	666	AHNRTCERYAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIP	720
		: : : : : : : : : : : : : : :	
Db	873	QEVQFCRFKDYREPPWAPNPYEF SKQYWFILSARLAFV IIFQNLVMFLSVLVDWMIPDIP	932
Qy	721	ESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPTV PKA-S	773
		: : : : : : : : : : : : : : :	
Db	933	TDISDQIKKEKSLLVDFFLKE----EHEKLKLMDEPALRSPGGGDRSR SRAASSAPSGQS	988
Qy	774	QL	775
Db	989	QL	990

RESULT 14

AEH82071

ID AEH82071 standard; protein; 913 AA.

XX

AC AEH82071;

XX

DT 15-JUN-2007 (revised)

DT 13-JUL-2006 (first entry)

XX

DE Human gnathodiaphyseal dysplasia protein, GDD1.

XX

KW Osteopathic; Gene therapy; bone disease; bone injury; bone resorption;

KW gnathodiaphyseal dysplasia; GDD1; BOND_PC; transmembrane protein 16E;

KW integral membrane protein GDD1; transmembrane protein 16E [Homo sapiens];

KW TMEM16E; GDD1; integral membrane protein GDD1 [Homo sapiens]; G05783;

KW G016020; G016021.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 356

FT /note= "Missense mutations in the coding sequence can

FT lead to substitution of this residue with either Arg or

FT Gly"

XX

PN JP2006121961-A.

XX

PD 18-MAY-2006.

XX

PF 28-OCT-2004; 2004JP-00313511.

XX

PR 28-OCT-2004; 2004JP-00313511.

XX

PA (UYTO-) UNIV TOKUSHIMA NAT UNIV CORP.

XX

PI Itakura M, Tsutsumi S, Kamata N, Inoue H;

XX

DR WPI; 2006-367194/38.

DR N-PSDB; AEH82070.

DR PC:NCBI; gi47106048.

DR PC:SWISSPROT; Q75V66.

XX

PT Novel gnathodiaphyseal dysplasia DNA, useful as diagnostic agent for bone

PT disease such as gnathodiaphyseal dysplasia, bone deficiency or bone-

PT resorption property disease.

XX

PS Claim 9; SEQ ID NO 2; 11pp; Japanese.

XX

CC The present invention relates to a human gnathodiaphyseal dysplasia (GDD)
 CC coding sequence (GDD1; AEH82070) and encoded protein (AEH82071). GDD1 is
 CC useful as a bone disease diagnostic agent, where the bone disease is GDD,
 CC bone deficiency and/or bone-resorption property disease, where the GDD
 CC disease causes hardening of bone, susceptibility to fracture, cement bone
 CC pathology of a lower jaw bone, etc. GDD1 is also useful in bone formation
 CC regeneration, hard tissue reconstruction, etc., and in research
 CC application.

CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 913 AA;

Query Match 34.3%; Score 1412.5; DB 11; Length 913;
 Best Local Similarity 39.2%; Pred. No. 1.2e-141;
 Matches 309; Conservative 148; Mismatches 259; Indels 73; Gaps 20;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE--LPNQASNWSAGLLAWLGIPN 58
 ::| :|| | :: : | | || ||| | :||:|:| :| : :| : :|
 Db 120 KRDSGDGRT--YFVKIHAPWEVLVTYAIEVLGIKMPIKESDIPRPKHTPISYVLGPVRLP- 176

Qy 59 VLLEVVPDVPPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEK-K 117
 | | | ||: :| :: || | | || | : | :|:|:| ||:| :| | |
 Db 177 -LSVKYPH--PEYFTAQFSRHRQELFLIED-QATFFPSSSRNRIVYYILSRCPFIEDGK 232

Qy 118 NLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLD 177
 || :|| | :|:| |||| : | | | | :| | | :||| : | ||||
 Db 233 KRFGIERLLNSNTYSSAYPLHDGQYWKPSEPPNP--TNERYTELHQNWARFSYFYKEQPLD 290

Qy 178 HVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSF 235
 :: |:|:| :|| :||| | | |||| | : | : : : | :| :
 Db 291 LIKNYYGEKIGIYFVFLGFYTEMLFFAAVVGGLACFIYGLLSMEHNTSSTEICDPEIGGQM 350

Qy 236 EMCPLCLD-CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAY 294
 |||| | :| | :| | : : ||| : ||||:| | :| | | :||:| :| |
 Db 351 IMCPLCDQVCDYWRLNSTCLASKFSHLFDNESTVFFAIFMGIWVTLFLEFWKQRQARLEY 410

Qy 295 RWDCSDYEDTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352
 || |:|:| : : ||:| | | :| | || | :| : : :
 Db 411 EWDLVDFEEEEQQQLQLRPEFEAMCKHRKLNVAVTKEMEPLYTRIPWYFLSGATVTLWM 470

Qy 353 AVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRI-----ASLTGS 394
 :|| |:|:|:| : : | :|| : ||||
 Db 471 SLVVTSMVAVIVYRL-----SVFATFASFMESDASLKQVKSFLTPQITTSLTGS 519

Qy 395 VVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFK 454
 :| : |||: | : : |:| :| || :| : |||:|:| ||||| | :|||
 Db 520 CLNFIVILILNFFYEKISAWITKMEIPRTYQEYESSLTLKMFLFQFVNFYSSCFYVAFFK 579

Qy	455	GRFVGYPGNYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWW	513
		: : : : : : :	
Db	580	GKFVGYPGKYTYLFWNRSEECDPGGCLIELTTQLTIIMTGKQIFGNIKEAIYPLALNWW	639
Qy	514	QKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPL	571
		: : :	
Db	640	-----RRRKARTNSEKLYSRWEQDHDLESFGPLGLFYEYLETVTQFGFVTLFVASFPL	692
Qy	572	APLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFS	631
		: : : : : : : : :	
Db	693	APLLALINNIVEIRVDAWKLTQYRRTVASKAHSIGVWQDILYGMAVLSVATNAFIVAFT	752
Qy	632	SDFLPRAYYRW----TRAHDLRGFLN-----FTLARAPSSFAAAHNHNR---TCRYRAFR--	677
		: : : : : : :	
Db	753	SDIIPRLVYYYAYSTNATQPMGTGYVNNLSVFLIADFPNHTAPSEKRDFITCRYRDYRYP	812
Qy	678	-DDDGHY--SQTYWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDIPESVEIKVKREYYLA	734
		: : : : : : : : : :	
Db	813	PDDENKYFHNMQFWHVLAAKMTFIIVMEHVFLVKFLLAWMIPDVPKDVVERIKREKLMT	872
Qy	735	KQALAENEV	743
		: : :	
Db	873	IKILHDFEL	881

RESULT 15

ABB62812

ID	ABB62812 standard; protein; 1219 AA.
XX	
AC	ABB62812;
XX	
DT	15-JUN-2007 (revised)
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 15228.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical; BOND_PC; CG6938-PA; CG6938-PA [Drosophila melanogaster];
KW	CG6938.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US009231.
XX	

PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL06915.
DR PC:NCBI; gi24663059.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 15228; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 1219 AA;

Query Match 33.4%; Score 1378.5; DB 4; Length 1219;
Best Local Similarity 37.8%; Pred. No. 8.5e-138;
Matches 304; Conservative 146; Mismatches 284; Indels 71; Gaps 19;

Qy 5 QDGNTTVHYALLSASWAVLCYYAEDLRLKLP-----LQELPNQASN 45
| | : : | : || : ||| | : :
Db 384 QSFNEKTFFLKIHL PWRLETRLAEVMNLKLPVKRFITISVKPSWDEENVL RNMQYW KDV 443

Qy 46 WSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRV NKLPRFLGSDNQDTFFTSTKRHQILFE 105
| | : : ||| : : | : |: | : | ||| :| : : :
Db 444 WQR-LTKKIQLDQTLLE---GETTFKAATANGNP EEQFIVKD-RATAFTSAQRSLMVMQ 497

Qy 106 ILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLN-QRQVLFQHW 164
:| :||: : : || :||: :| |||:| : : | : : : | :||:| |
Db 498 VLIRTPFDES DRS--GIRRLMNDGTYLGC FPLHEGRY----DRPHSSGISLDRRVLYQTW 551

Qy	165	ARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFS--	222
Db	552	AHPSQWYKKQPLCLVRKYFGDKIALYFCWLGFYTEMLVYPAVVGTLCFIYGLATLESEDN	611
Qy	223	IPTQELCG--SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAV	279
Db	612	TPSKEICNEYGTGNITLCPLCDKACSYQRLSESCLF SRLTYLFDNPSTVFFAIFMSFWAT	671
Qy	280	LLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRAR	339
Db	672	TFLELWKRKQSVLVWEWDLHNV-DMDEENRPEFETNATTFRMNPVTREKEPYMSTWNRSI	730
Qy	340	RMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAWASRIASLTGSVVNLV	399
Db	731	RFVITGSAVLFMISVVL SAVLGTILYRITLVSVIYGGGGFFVKEHAKLFTSVTAALINLV	790
Qy	400	FILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVG	459
Db	791	VIMILTRIYHRMAIKLTNLENPRTHTEYEDSYTFKIFFFEFMNFYSSLIYIAFFKGRFFD	850
Qy	460	YPGNYHT---LFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQK	515
Db	851	YPGDDQARKSEFFRLKNDICDPAGCLSELCIQLAIIMVGKQCWNNFMEYLFPKFWNWWR-	909
Qy	516	FRLRSKKRKAGASAGASQGPWEDDYELV-PCE-GLFDEYLEMVLQFGFVTIFVAACPLAP	573
Db	910	---QRKHKQATKDESHLHMAWEQDYHMQDPGRLALFDEYLEMILQYGFVTLFVAAFPLAP	966
Qy	574	LFALLNNWVEIRLDARKEFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSD	633
Db	967	LFALLNNVAEIRLDAYKMVTQARRPLAERVEDIGAWYGILRIITYTAVVSNAFVIAYTSD	1026
Qy	634	FLPRAYYR--WTRAHDLRGFLNFTLA-----RAPSSFAAAHNRTCryRAFRDDDDGH	682
Db	1027	FIPRMVYKFVYSEHTLAGYIEHSLSIFNTSDYKEEWGASVSEKDPDTCQYRGYRNGPKD	1086
Qy	683	Y-----SQTYNLLAIRLAFVIVFEHVVF SVGRLLDLLVPDIPESVEIKVKREYYLAKQA	737
Db	1087	YEPYGLSPHYWHVFAARLAFVVVFEHVVFVITGIMQFIIPDVPSEVKTQM QREQLLAKEA	1146
Qy	738	LAENEVLFGTNGTKDEQPKGSELSS	762
Db	1147	KYQ-----HGIKRAQGDSQDIMS	1164

Search completed: June 24, 2008, 15:22:07
Job time : 273 secs

SCORE 0